

(i) APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Tang, Y. Tom
Yue, Henry
Corley, Neil C.

(iii) NUMBER OF SEQUENCES: 3

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEO for Windows Version 2.0

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(A) APPLICATION NUMBER:
(B) FILING DATE:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0484 US

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(A) LENGTH: 619 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) LIBRARY: SMCANOT01
(B) CLONE: 2479739

Met	Ser	Gly	Leu	Val	Leu	Gly	Gln	Arg	Asp	Glu	Pro	Ala	Gly	His	Arg
1				5					10					15	
Leu	Ser	Gln	Glu	Glu	Ile	Leu	Gly	Ser	Thr	Arg	Leu	Val	Ser	Gln	Gly
			20					25					30		
Leu	Glu	Ala	Leu	Arg	Ser	Glu	His	Gln	Ala	Val	Leu	Gln	Ser	Leu	Ser
		35					40					45			
Gln	Thr	Ile	Glu	Cys	Leu	Gln	Gln	Gly	Gly	His	Glu	Glu	Gly	Leu	Val
50						55					60				

[illegible]

595 600 605
 Ser Ala Ser Thr Met Asp Leu Ser Ser Ser Ser
 610 615

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
 (B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAAGTGGT GAAAGAAGGG GTGGGAACGC TGGACTTCTG GACTTTGGGC AGGGCAGATC 60
 CTCTGACTCT CTGGCTGCAG AACAGTTTCT TCCGTGCTCT GGCCTGAGTG CCCACAGGCC 120
 AGGGGCCTCT GCTCTGTACA CAGACCGGGC AAGGTCCCCC AGGCCAGGAT GTCAGGCCTG 180
 GTGTTGGGGC AGCGGGATGA GCCTGCAGGC CACCGGCTCA GCCAAGAGGA GATCCTGGGG 240
 AGCACACGGC TGGTCAGCCA AGGGCTAGAG GCCCTACGCA GTGAACACCA GGCCGTGCTG 300
 CAAAGCCTGT CCCAGACCAT TGAGTGTCTG CAGCAGGGAG GCCATGAGGA AGGGCTGGTG 360
 CATGAGAAGG CCCGGCAGCT TCGCCGTTCT ATGGAAAACA TTGAGCTCGG GCTGAGTGAG 420
 GCCCAGGTGA TGCTGGCTCT AGCCAGCCAC CTGAGCACAG TGGAGTCGGA GAAACAGAAG 480
 CTGCGGGCTC AGGTGCGGCG GCTATGCCAG GAGAACCAGT GGCTGCGGGA TGAGCTGGCT 540
 GGCACCCAGC AGCGGCTACA GCGCAGTGAA CAGGCTGTGG CTCAGCTGGA GGAGGAAAAG 600
 AAGCACCTGG AGTTCCTGGG GCAGCTGCGG CAGTATGATG AGGATGGACA TACCTCGGAG 660
 GAGAAAGAAG GCGATGCCAC CAAGGATTCC CTGGATGACC TCTTTCCTAA TGAGGAGGAA 720
 GAGGACCCCA GCAATGGCTT GTCCCGTGGT CAAGGTGCTA CAGCAGCTCA GCAGGGTGGA 780
 TATGAGATCC CAGCAAGGTT GCGGACGTTG CACAACCTGG TGATCCAGTA CGCAGCCCAA 840
 GGTGCTATG AGGTGGCCGT GCCACTCTGT AAGCAGGCAC TAGAGGACCT GGAGCGCACA 900
 TCAGGCCGTG GCCACCCTGA TGTCGCCACC ATGCTCAACA TCCTTGCTTT GGTGTATCGT 960
 GACCAGAATA AGTATAAGGA AGCTGCCCAC CTGCTGAATG ATGCCCTTAG CATCCGGGAG 1020
 AGCACCTTGG GACCTGACCA TCCTGCTGTG GCTGCCACAC TCAACAATTT GGCTGTGCTC 1080
 TATGGCAAAA GGGGCAAGTA CAAGGAGGCA GAGCCTCTGT GCCAGCGGGC ACTGGAGATT 1140
 CGAGAAAAGG TCCTGGGCAC GAATCATCCA GATGTGGCAA AACAGCTGAA CAACCTGGCC 1200
 CTCTTGTCGC AAAACCAGGG CAAGTATGAG GCCGTGGAAC GCTACTACCA GCGAGCACTG 1260
 GCCATCTACG AGGGGCAGCT GGGGCCGGAC AACCCTAATG TAGCCCGGAC CAAGAACAAC 1320
 CTGGCTTCCT GTTACCTGAA ACAGGGCAAA TATGCTGAGG CTGAGACACT ATACAAAGAG 1380
 ATCCTGACCC GTGCCCATGT ACAGGAGTTT GGGTCTGTGG ATGATGACCA CAAGCCCATC 1440
 TGGATGCATG CAGAGGAGCG GGAGGAAATG AGCAAAAGCC GGCACCATGA GGGTGGGACA 1500
 CCCTATGCTG AGTATGGAGG CTGGTACAAG GCCTGCAAAG TGAGCAGCCC CACAGTGAAC 1560
 ACTACTCTGA GAAACCTGGG AGCTCTGTAT AGGCGCCAGG GAAAGCTGGA GGCTGCTGAG 1620
 ACCCTGGAGG AATGTGCCCT GCGGTCCCGG AGACAGGGCA CTGACCCTAT CAGCCAGACG 1680
 AAGGTGGCAG AGCTGCTTGG GGAGAGTGAT GGTAGAAGGA CCTCCCAGGA GGGCCCTGGA 1740
 GACAGTGTGA AATTCGAGGG TGGTGAAGAT GCTTCTGTGG CTGTGGAGTG GTCCGGGGAT 1800
 GGCAGTGGGA CCCTGCAGAG GAGTGGCTCT CTTGGCAAGA TCCGGGATGT GCTCCGCAGA 1860
 AGCAGTGAAC TCTTGGTGAG GAAGCTCCAG GGGACTGAGC CTCGGCCCTC CAGCAGCAAC 1920
 ATGAAGCGAG CAGCCTCCTT GAACTATCTG AACCAACCTA GTGCAGCACC CCTCCAGGTC 1980
 TCCCGGGGCC TCAGTGCCAG CACCATGGAC CTCTCTTCAA GCAGCTGACA TTCAACCCGG 2040
 CCCCCAGGTC TGCTGGGTCC CCCCACCCCC ACAGCCCTCA CAGCATTCCC CATTGCTCCT 2100
 GGCTCTTCCC CACCCCTAGG TGGGACAGTG AAGGGGAGCA GTTTAACCAG AAGATTGCTG 2160
 CTGCCCTTAG GGTCTCAGCT CCCTCCTCAG GAATCCCTCT TAGGAAGGAC CCTCAGGACA 2220
 CCCTCTCTGC ACCCTGTGGT CCTCTAGAGT AGCTAGCTCT GAGGCCCCAA GGTGGGTACA 2280
 AAGCAGGTAT GGCCCTCAGA GATGCAGCCT GCTGCTGGCT TTTCAGTCAG AGGGTTGGGG 2340
 GCTGGCCAGC CAAGCTGCCT TGCCCTGGCC GCTCTTACTC CCTCCCTCTG CTGTCTCACT 2400
 TCAGGTCCAT GTATTTCACT TTTCTTAAAT AAAAGAATCA GTNCTTNTNT NNG 2453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 307085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
1 5 10 15
Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
20 25 30
Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
35 40 45
Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
50 55 60
Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
65 70 75 80
Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
85 90 95
Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
100 105 110
Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
115 120 125
Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
130 135 140
Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Ile Ser Pro Ser
145 150 155 160
Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
165 170 175
Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
180 185 190
Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
195 200 205
Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
210 215 220
Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
225 230 235 240
Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile
245 250 255
Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
260 265 270
Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
275 280 285
His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
290 295 300
Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
305 310 315 320
Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
325 330 335
Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
340 345 350
Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
355 360 365
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
370 375 380
Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
385 390 395 400
Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
405 410 415
Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
420 425 430
Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
435 440 445
Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys
450 455 460
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
465 470 475 480
Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn

				485					490					495			
Val	His	Lys	Gln	Arg	Val	Ala	Glu	Val	Leu	Asn	Asp	Pro	Glu	Asn	Met		
			500					505					510				
Glu	Lys	Arg	Arg	Ser	Arg	Glu	Ser	Leu	Asn	Val	Asp	Val	Val	Lys	Tyr		
		515					520					525					
Glu	Ser	Gly	Pro	Asp	Gly	Gly	Glu	Glu	Val	Ser	Met	Ser	Val	Glu	Trp		
	530					535					540						
Asn	Gly	Gly	Val	Ser	Gly	Arg	Ala	Ser	Phe	Cys	Gly	Lys	Arg	Gln	Gln		
545					550					555					560		
Gln	Gln	Trp	Pro	Gly	Arg	Arg	His	Arg									
				565													

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